1600

RAW SEQUENCE LISTING   DATE: 06/28/2002
PATENT APPLICATION: US/09/658,835C   TIME: 11:08:48

Input Set : **A:\PTO.PG.txt**
Output Set: **N:\CRF3\06282002\I658835C.raw**

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 3 <110> APPLICANT: Duvick, Jonathan P.
 4         Gilliam, Jacob T.
 5         Maddox, Joyce R.
 6         Rao, Aragula Gururaj
 7         Crasta, Oswald R.
 8         Folkerts, Otto
10 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase Polynucleotides and Related
Polypeptides and
11         Methods of Use
13 <130> FILE REFERENCE: 1134R
15 <140> CURRENT APPLICATION NUMBER: US 09/658,835C
16 <141> CURRENT FILING DATE: 2000-09-08
18 <150> PRIOR APPLICATION NUMBER: US 60/092,936
19 <151> PRIOR FILING DATE: 1998-07-25
21 <150> PRIOR APPLICATION NUMBER: US 60/135,391
22 <151> PRIOR FILING DATE: 1999-05-21
24 <150> PRIOR APPLICATION NUMBER: US 09/352,159
25 <151> PRIOR FILING DATE: 1999-07-12
27 <150> PRIOR APPLICATION NUMBER: US 09/352,168
28 <151> PRIOR FILING DATE: 1999-07-12
30 <160> NUMBER OF SEQ ID NOS: 53
32 <170> SOFTWARE: PatentIn version 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 372
36 <212> TYPE: DNA
37 <213> ORGANISM: Exophiala spinifera
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40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (346)..(346)
42 <223> OTHER INFORMATION: n = A, T, C, or G
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50 attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtca cagctcgatt   180
52 ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct   240
54 tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg   300
56 gtgaaaatgt caaggtggga tacaaggttg tcggtaacga aaccancacc tttttgcttc   360
58 ggaacacggc gc                                                       372
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62 <211> LENGTH: 182
63 <212> TYPE: DNA
64 <213> ORGANISM: Exophiala spinifera
66 <400> SEQUENCE: 2
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W--> (line 56)

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69 tacaaggttg tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc     120
71 gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc     180
73 ac                                                                    182
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77 <211> LENGTH: 29
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Designed oligo for 3' RACE N21965 (Exophiala spinifera)
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88 <210> SEQ ID NO: 4
89 <211> LENGTH: 28
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91 <213> ORGANISM: Artificial Sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Designed oligo for 5' RACE 21968 (Exophiala spinifera)
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102 <212> TYPE: DNA
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107 <222> LOCATION: (1)..(1386)
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113 1               5                   10                  15
115 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt      96
116 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
117             20                  25                  30
119 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt      144
120 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
121         35                  40                  45
123 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac      192
124 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
125     50                  55                  60
127 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag      240
128 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
129 65                  70                  75                  80
131 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac      288
132 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
133             85                  90                  95
135 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag      336
136 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
137             100                 105                 110
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139 gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc      384
140 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
141         115                 120                 125
143 gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg      432
144 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
145         130                 135                 140
147 ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg      480
148 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
149 145             150                 155                 160
151 cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt      528
152 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
153             165                 170                 175
155 gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag      576
156 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
157         180                 185                 190
159 agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg      624
160 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
161         195                 200                 205
163 cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg      672
164 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
165         210                 215                 220
167 tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct      720
168 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
169 225             230                 235                 240
171 gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc      768
172 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
173             245                 250                 255
175 gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg      816
176 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
177             260                 265                 270
179 tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca      864
180 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
181         275                 280                 285
183 ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta      912
184 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
185         290                 295                 300
187 tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa      960
188 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
189 305             310                 315                 320
191 tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc      1008
192 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
193             325                 330                 335
195 gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg      1056
196 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
197             340                 345                 350
199 aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac      1104
200 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
201         355                 360                 365
203 caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg      1152
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204 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
205     370               375               380
207 gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga    1200
208 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
209 385               390               395               400
211 gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg    1248
212 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
213               405               410               415
215 gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg    1296
216 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
217               420               425               430
219 tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa    1344
220 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
221               435               440               445
223 cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag        1389
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225     450               455               460
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230 <212> TYPE: PRT
231 <213> ORGANISM: Exophiala spinifera
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239 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
240               20               25               30
243 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
244     35               40               45
247 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
248     50               55               60
251 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
252 65               70               75               80
255 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
256               85               90               95
259 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
260               100               105               110
263 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
264               115               120               125
267 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
268     130               135               140
271 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
272 145               150               155               160
275 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
276               165               170               175
279 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
280               180               185               190
283 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
284     195               200               205
287 Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
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288      210                    215                    220
291  Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
292  225                230                    235                    240
295  Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
296                245                    250                    255
299  Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
300                260                    265                    270
303  Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
304           275                    280                    285
307  Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
308      290                    295                    300
311  Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
312  305                310                    315                    320
315  Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
316                325                    330                    335
319  Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
320           340                    345                    350
323  Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
324           355                    360                    365
327  Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
328      370                    375                    380
331  Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
332  385                390                    395                    400
335  Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
336                405                    410                    415
339  Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
340           420                    425                    430
343  Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
344           435                    440                    445
347  Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
348      450                    455                    460
351  <210> SEQ ID NO: 7
352  <211> LENGTH: 1442
353  <212> TYPE: DNA
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356  <220> FEATURE:
357  <221> NAME/KEY: CDS
358  <222> LOCATION: (1)..(645)
359  <223> OTHER INFORMATION:
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362  <221> NAME/KEY: Intron
363  <222> LOCATION: (646)..(698)
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368  <222> LOCATION: (699)..(1439)
369  <223> OTHER INFORMATION:
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 346
Seq#:39; N Pos. 649
Seq#:40; Xaa Pos. 216